

FIG. 1A

10 30 50
 GAATTCGGCACGAGCTGAGGGGTGAGCCAAGCCCTGCCATGTAGTGCACGCAGGACATCA
 70 90 110
 ACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGTCACTTATTCTAAAGGCCCCAA
 130 150 170
 CCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAGGGAGCAGTCACGCCTTAC
 M D D S T E R E Q S R L T
 190 210 230
 TTCTTGCCCTTAAGAAAAGAGAAGAAATGAACTGAAGGAGTGTGTTTCCATCCTCCCACG
 S C L K K R E E M K L K E C V S I L P R
 250 270 290
 GAAGGAAAGCCCCCTCTGTCCGATCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCTTGCT
 K E S P S V R S S K D G K L L A A T L L
 310 330 350
 GCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTTCTACCAGGTGGCCGCCCTGCA
L A L L S C C L T V V S F Y O V A A L Q
 370 390 410
 AGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGCCAGC
 G D L A S L R A E L Q G H H A E K L P A
 430 450 470
 AGGAGCAGGAGCCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGACTGAA
 G A G A P K A G L E E A P A V T A G L K
 490 510 530
 AATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCG
 I F E P P A P G E G N S S Q N S R N K R
 550 570 590
 TGCCGTTTCAGGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAGACAG
 A V Q G P E E T V T Q D C L Q L I A D S

FIG. 1B

```

        610                630                650
TGAAACACCAACTATACAAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAA
  E  T  P  T  I  Q  K  G  S  Y  T  F  V  P  W  L  L  S  F  K
        670                690                710
AAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTTACTT
  R  G  S  A  L  E  E  K  E  N  K  I  L  V  K  E  T  G  Y  F
        730                750                770
TTTTATATATGGTCAGGTTTTATATACTGATAAGACCTACGCCATGGGACATCTAATTCA
  F  I  Y  G  Q  V  L  Y  T  D  K  T  Y  A  M  G  H  L  I  Q
        790                810                830
GAGGAAGAAGGTCCATGTCTTTGGGGATGAATTGAGTCTGGTGACTTTTGTTCGATGTAT
  R  K  K  V  H  V  F  G  D  E  L  S  L  V  T  L  F  R  C  I
        850                870                890
TCAAAATATGCCTGAAACACTACCCAATAATTCCTGCTATTCAGCTGGCATTTGCAAAACT
  Q  N  M  P  E  T  L  P  N  N  S  C  Y  S  A  G  I  A  K  L
        910                930                950
GGAAGAAGGAGATGAACTCCAATTGCAATACCAAGAGAAAATGCACAAATATCACTGGA
  E  E  G  D  E  L  Q  L  A  I  P  R  E  N  A  Q  I  S  L  D
        970                990               1010
TGGAGATGTCACATTTTTTTGGTGCAATTGAAACTGCTGTGACCTACTTACACCATGTCTGT
  G  D  V  T  F  F  G  A  L  K  L  L
       1030                1050                1070
AGCTATTTTCCCTCCCTTTCTCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATACCAA
   1090                1110                1130
AAAAAAAAAAAAAAAAAAAAAAAAAGTAGTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
   1150                1170
AAAAAAAAAAAAAAAAAAAAAAAAACTCGGAGGGGG

```

FIG. 2A

10 30 50
GAATTCGGCACGAGCTCCAAAGGCCTAGACCTTCAAAGTGCTCCTCGTGAATGGATGAG
M D E
70 90 110
TCTGCAAAGACCCTGCCACCACCGTGCCTCTGTTTTTGCTCCGAGAAAGGAGAAGATATG
S A K T L P P P C L C F C S E K G E D M
130 150 170
AAAGTGGGATATGATCCCATCACTCCGCAGAAGGAGGAGGGTGCCTGGTTTGGGATCTGC
K V G Y D P I T P Q K E E G A W F G I C
190 210 230
AGGGATGGAAGGCTGCTGGCTGCTACCCTCCTGCTGGCCCTGTTGTCCAGCAGTTTCACA
R D G R L L A A T L L L A L L S S S F T
250 270 290
GCGATGTCCTTGTACCAGTTGGCTGCCTTGCAAGCAGACCTGATGAACCTGCGCATGGAG
A M S L Y O L A A L Q A D L M N L R M E
310 330 350
CTGCAGAGCTACCGAGGTTTCAGCAACACCAGCCGCCGCGGTGCTCCAGAGTTGACCGCT
L Q S Y R G S A T P A A A G A P E L T A
370 390 410
GGAGTCAAACCTCCTGACACCGGCAGCTCCTCGACCCCACAACTCCAGCCGCGGCCACAGG
G V K L L T P A A P R P H N S S R G H R
430 450 470
AACAGACGCGCTTTCAGGGACCAGAGGAAACAGAACAAGATGTAGACCTCTCAGCTCCT
N R R A F Q G P E E T E Q D V D L S A P
490 510 530
CCTGCACCATGCCTGCCTGGATGCCGCCATTCTCAACATGATGATAATGGAATGAACCTC
P A P C L P G C R H S Q H D D N G M N L
550 570 590
AGAAACATCATTTCAAGACTGTCTGCAGCTGATTGCAGACAGCGACACGCCGACTATACGA
R N I I Q D C L Q L I A D S D T P T I R

FIG. 2B

610 630 650
 AAAGGAACTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGAGGAAATGCCTTGGAG
 K G T Y T F V P W L L S F K R G N A L E
 670 690 710
 GAGAAAGAGAACAAAATAGTGGTGAGGCAAACAGGCTATTTCTTCATCTACAGCCAGGTT
 E K E N K I V V R Q T G Y F F I Y S Q V
 730 750 770
 CTATACACGGACCCCATCTTTGCTATGGGTCATGTCATCCAGAGGAAGAAAGTACACGTC
 L Y T D P I F A M G H V I Q R K K V H V
 790 810 830
 TTTGGGGACGAGCTGAGCCTGGTGACCCTGTTCCGATGTATTCAGAATATGCCCAAACA
 F G D E L S L V T L F R C I Q N M P K T
 850 870 890
 CTGCCCCAACAAATTCCTGCTACTCGGCTGGCATCGCGAGGCTGGAAGAAGGAGATGAGATT
 L P N N S C Y S A G I A R L E E G D E I
 910 930 950
 CAGCTTGCAATTCCTCGGGAGAATGCACAGATTTACGCAACGGAGACGACACCTTCTTT
 Q L A I P R E N A Q I S R N G D D T F F
 970 990 1010
 GGTGCCCTAAAACTGCTGTAACCTCACTTGCTGGAGTGCGTGATCCCCCTCCCTCGTCTTC
 G A L K L L
 1030 1050 1070
 TCTGTACCTCCGAGGGAGAAACAGACGACTGGAAAACTAAAAGATGGGGAAAGCCGTCA
 1090 1110 1130
 GCGAAAGTTTCTCGTGACCCGTTGAATCTGATCCAAACCAGGAAATATAACAGACAGCC
 1150 1170 1190

FIG. 3A

	1		50
Hagp3	MDDSTER.EQ	SRLTSLCKKR	EEMKLKECVS ILPRKESPSV RSSKDGKLLA
Magp3	MDESAKTLPP	PCLCFCSEKG	EDMKVGYPDPI TPQKEEGAWF GICRDGRLLA
cons	MD.S.....	..L..C..K.	E.MK.....E.... ..DG.LLA
	51		100
Hagp3	<u>ATLLLLALLSC</u>	<u>CLTVVSFYOV</u>	<u>AALQGDLASL</u> RAELQGHAE KLPAGAGAPK
Magp3	<u>ATLLLLALLSS</u>	<u>SFTAMSLYQL</u>	<u>AALQADLMNL</u> RMELQSYRGS ATPAAAGAPE
cons	ATLLLLALLS.	..T..S.YQ.	AALQ.DL..L R.ELQ..... ..PA.AGAP.
	101		150
Hagp3	AGLEEAPAVT	AGLKIFEPPA	PGEKNSSQNS RNKRAVQGPE ET.....
Magp3LT	AGVKLLTPAA	PRPHNSSRGH RNRRAFQGPE ETEQDVDSL
consT	AG.K...P.A	P...NSS... RN.RA.QGPE ET.....
	151	B	200
Hagp3VTQDCLO <u>LIADSETPTI</u> QKGSYTFVPW
Magp3	PPAPCLPGCR	HSQHDDNGMN	LRNIIQDCLO <u>LIADSDTPTI</u> RKGTYTFVPW
consQDCLO LIADS.TPTI .KG.YTFVPW

FIG. 3B

	B'	C'	C	D	E	250
Hagp3	<u>LLSEFKRG</u> SAL	<u>EEKENKIL</u> VK	ETGYFFFIYGO	<u>VL</u> YTDKTYAM	<u>GH</u> LIQRKKVH	
Magp3	<u>LLSEFKRG</u> NAL	<u>EEKENKI</u> VVR	QTGYFFFIYSO	<u>VL</u> YTDPIFAM	<u>GH</u> VIQRKKVH	
cons	LLSEFKRG.AL	EEKENKI.V.	.TGYYFFIY.Q	VLYTD...AM	GH.IQRKKVH	
	F	G	H			300
Hagp3	<u>VFGDEL</u> SLVT	<u>LFRCIQ</u> NMPE	<u>TL</u> PNNSCYSA	<u>GIAK</u> LEEGDE	<u>LO</u> LAIPRENA	
Magp3	<u>VFGDEL</u> SLVT	<u>LFRCIQ</u> NMPK	<u>TL</u> PNNSCYSA	<u>GIA</u> RLEEGDE	<u>IOL</u> AIPRENA	
cons	VFGDELSLVT	LFRCIQNMP.	<u>TL</u> PNNSCYSA	GIA.LEEGDE	.QLAIPRENA	
	I					317
Hagp3	<u>QISLDG</u> DVTF	<u>FGAL</u> KLL				
Magp3	<u>QISRNG</u> DDTF	<u>FGAL</u> KLL				
cons	QIS..GD.TF	FGALKLL				

FIG. 4A

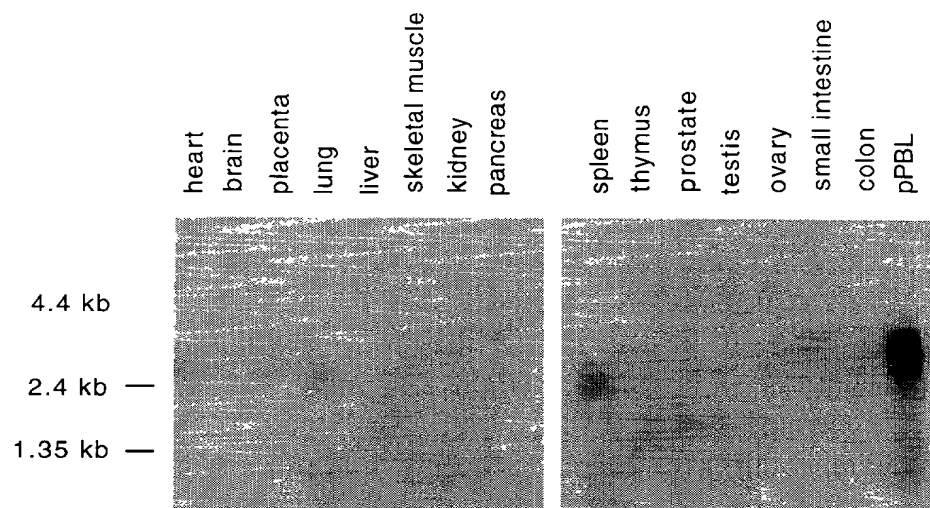


FIG. 4B

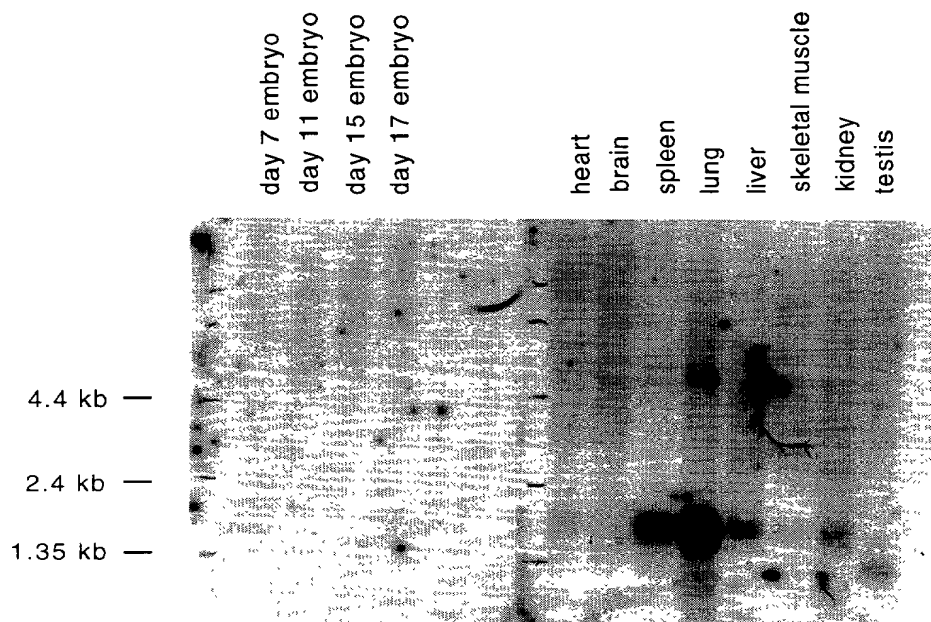


FIG. 5A

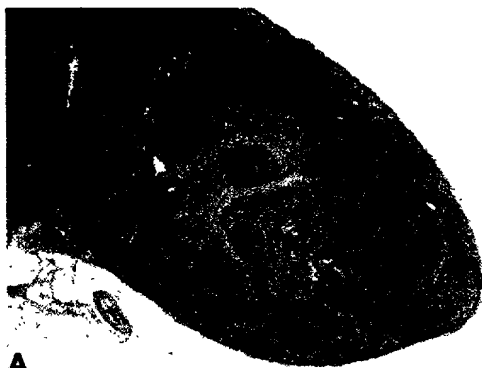


FIG. 5B

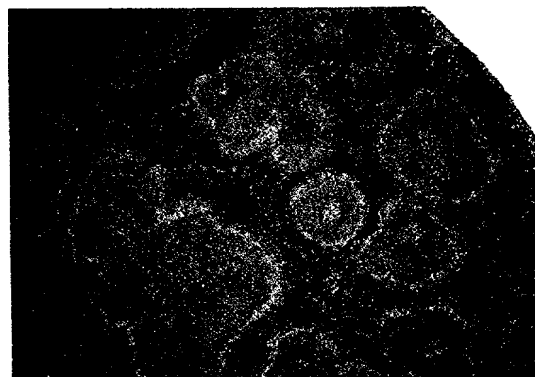


FIG. 5C

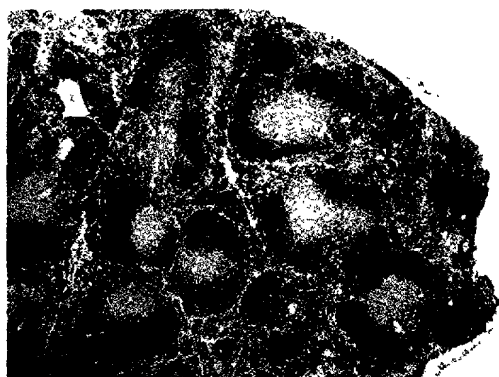


FIG. 5D

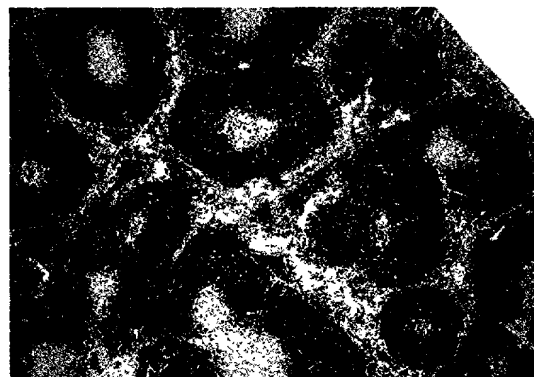


FIG. 5E

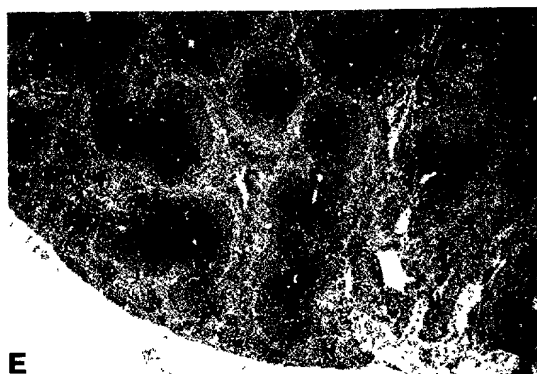


FIG. 5F

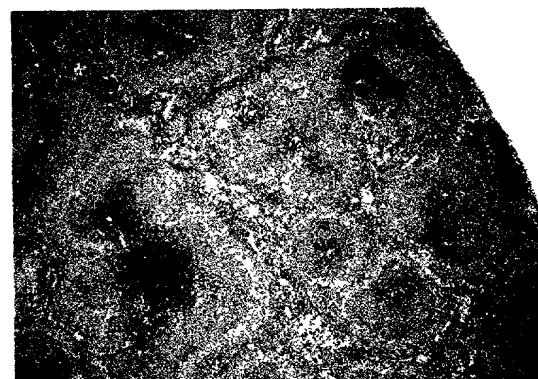


FIG. 6A

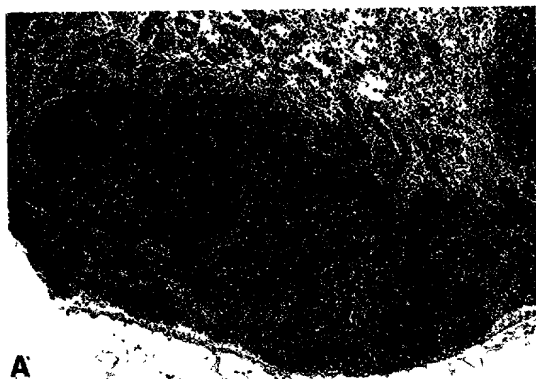


FIG. 6B



FIG. 6C

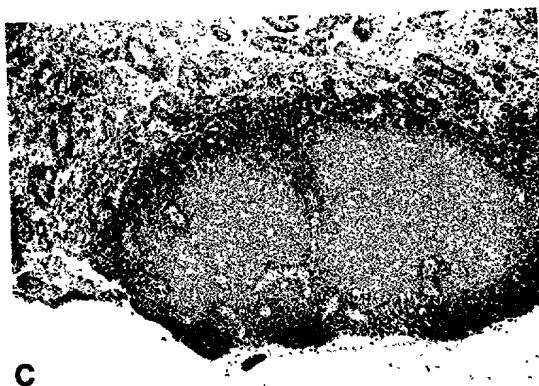


FIG. 6D

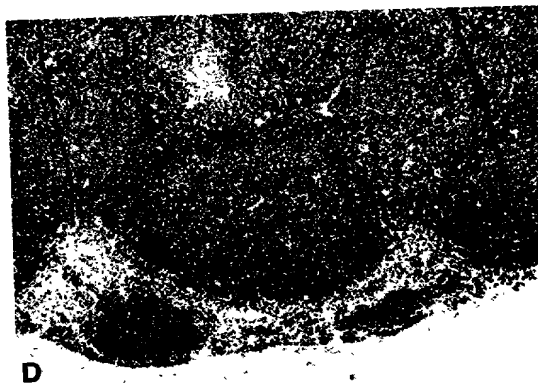


FIG. 6E



FIG. 6F

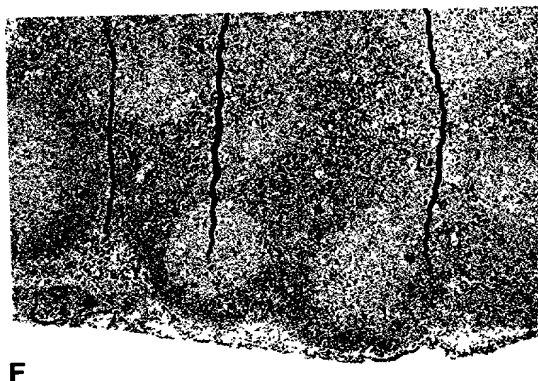


FIG. 7A



A

FIG. 7B



B

FIG. 7C



C

FIG. 7D



D

FIG. 7E



E

FIG. 7F



F

FIG. 8A

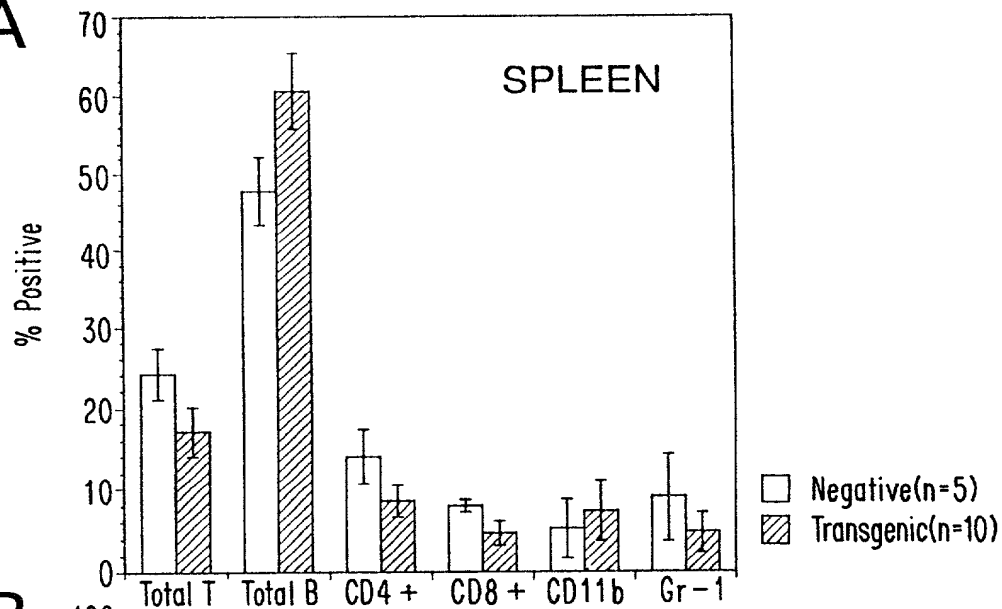


FIG. 8B

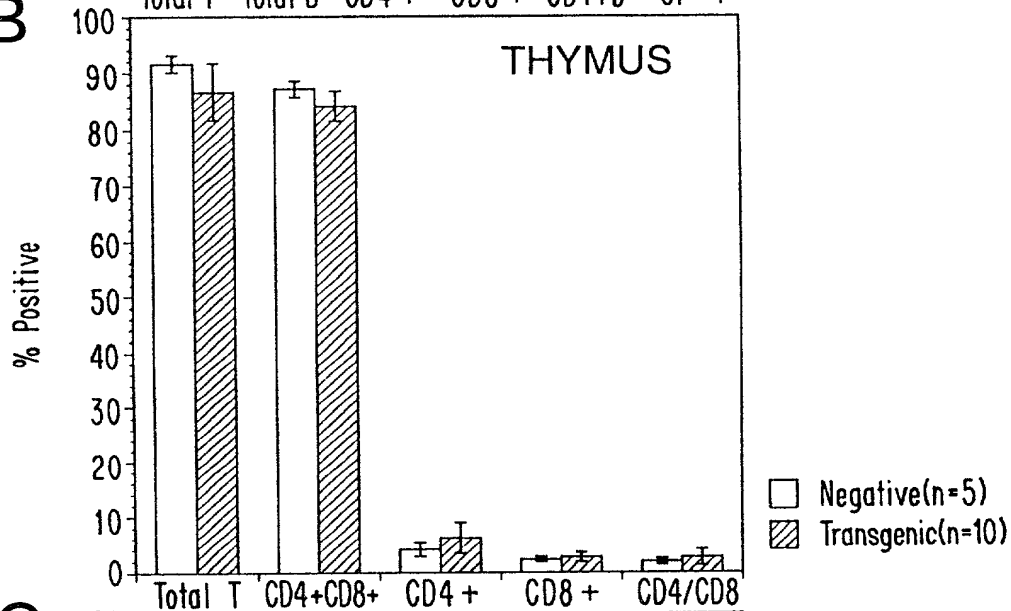


FIG. 8C

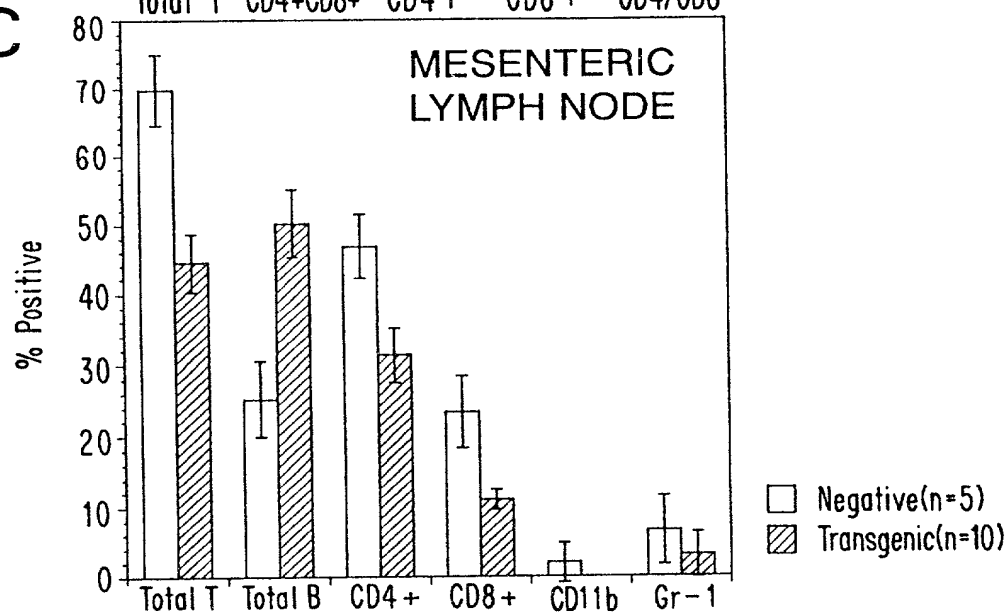


FIG. 9A

	B	B/B' loop	B'	C'	C	D	D/E loop	E	Consensus
	-----+PAAHLT--P-----	-----L-W-----	-----A-LS-GV-L-N-----	-----LVW-----	-----GLYFIYSQV-F+GQ-CP-----	-----V-L			Human FasL
139-	EKKELKVAHLTGKSN-----	-----SRS-MPLEWEDTYGI-----	-----VLLS-GVKYKK-----	-----GGLVINETGLYFVYSKVYFRGQSCN-----	-----NLPL				Mouse FasL
137-	EKKEPSVAHLTGKSN-----	-----SRS-IPLEWEDTYGT-----	-----ALIS-GVKYKK-----	-----GGLVINETGLYFVYSKVYFRGQSCN-----	-----NQPL				Rat FasL
136-	ETKKPRVAHLTGKSN-----	-----SRS-IPLEWEDTYGT-----	-----ALIS-GVKYKK-----	-----GGLVINEAGLYFVYSKVYFRGQSCN-----	-----SQPL				Human CD40L
116-	GDQNPQIAAHVISEASS-----	-----KTT-SVLQWAEKGY--TMSNNLVTLENG-KQLTVKRQGLYIYAQVTFCSNREA-----	-----SSQAPF						Mouse CD40L
115-	GDQNPQIAAHVISEANS-----	-----NAA-SVLQWAKKGY--TMSKSNLVMLENG-KQLTVKRQGLYIYVTVTFCSNREP-----	-----SSQAPF						Human AGP3
142-	-----VTQDCIQLIADSETPTIQ-----	-----KGSY--TFVPWLLSFKR-GSALE-----	-----EKEN--KIL-VKETGYFIYQVLYT-DKT-----	-----YAMGHL					Mouse AGP3
163-	LRNIIQDCIQLIADSDTPTIR-----	-----KGTY--TFVPWLLSFKR-GNALE-----	-----EKEN--KI-VWRQTGYFIYSQVLYT-DPI-----	-----FAMGHV					Mouse OPGL
157-	GKPEAQFAHLTINAASIP-----	-----SGSHKVTLSWYHNRGW--AKISN-MTSLNG-K-LRVNODGFYLYANICFRHHETS-----	-----GSVPTD						Human OPGL
158-	SKLEAQFAHLTINATDIP-----	-----SGSHKVTLSWYHNRGW--AKISN-MTFSNG-K-LIVNQDGFYLYANICFRHHETS-----	-----GDLATE						Human TRAIL
116-	ERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGH-SFLSN-LHLRNG-E-LVIEQEGLYIYSQTYFRFQEAEDASKVSKD-								Mouse TRAIL
120-	GGRPQVAAHITGITRRSNSALIPISKDGKTLGQKIESWESSRKGH-SFLNH-VLFRNG-E-LVIEQEGLYFIICQLQFLVQ-CP-----								Human CD30L
92-	RAPFKKSWAYLQVAKH-----	-----LNK-TKLSWNKDG-----	-----ILH-GVRYQD--GNLVIQFPGLYFIICQLQFLVQ-CP-----						Mouse CD30L
97-	STPSKKSWAYLQVSKH-----	-----LNN-TKLSWNEDG-----	-----TIH-GLIYQD--GNLIVQFPGLYFIICQLQFLVQ-CS-----						Human Lytβ
82-	DLSPGLPAAHLIGAP-----	-----LKGQ-GLGWETTKEQ--AFLTSGTQFSDA-EGALALPDQGLYLYCLVGYRGRAPPGGGDPQGRSV							Mouse Lytβ
148-	DLNPGLPAAHLIGAW-----	-----MSGQ-GLSWEASQEE--AFLRSGAQFSPT-HGLALPDQGVYLYCHVGYRGRTPPA-GRSRARSL							Human TNFβ
57-	AHSTLKPAAHLIGDP-----	-----SKQNS-LLWRANTDR--AFLQDGFSLN--NSLLVPTSGIYFVYSQVWFSKGKAYSPKATSSPLYL							Mouse TNFβ
54-	THGILKPAAHLVGYP-----	-----SKQNS-LLWRASTDR--AFLRHGFSLN--NSLLIPTSGIYFVYSQVWFSGESCPRAIPTPIYL							Human TNFα
82-	RTPSDKPVAVHVVANP-----	-----QAEQG-QWLNNRRAN--ALLANGVELRD--NQLVVPSEGLYIYSQVLFKGQGCIP-----	-----STHVLL						Mouse TNFα
85-	QNSDDKPVAVHVVANH-----	-----QVEEQ-LEWLSQRAN--ALLANGMDLKD--NQLVVPADGLYLYVYSQVLFKGQGCIP-----	-----DYVLL						

FIG. 9B

E	E/F loop	F	F/G loop	G	H	H/I loop	I
208-	-H-V---V-----YP-----LLS-----T---C-----W-S-YLGGVF-L--GD-LYVNV---S---F-----TFFGLFKL						-281
206-	SHKVYMRNS-----KYPQDLVMMEGKMMSYC-----TTGQMWARSYYLGAVENLTSAHLYVNVSELSLVNFEESQ-TFFGLYKL						-279
205-	NHKVYMRNS-----KYPEDLVIMEEKRLNYC-----TTGQIWAHSSYLGAVENLTSAHLYVNIQSLSLINFEEK-TFFGLYKL						-278
190-	SHKVYMRNF-----KYPGDLVIMEEKKLNYC-----TTGQIWAHSSYLGAVENLTVAHLYVNIQSLSLINFEEK-TFFGLYKL						-261
189-	IASLCLKS-----PGRFERILLRAANTHSSAKPC-----GQSIHLGGVFELQPGASVFVNVTDPQSQVSHGTGF-TSFGLLKL						-260
212-	IVGLWLKP-----SIGSERILLKAANTHSSQLC-----EQQSVHLGGVFELQAGASVFVNVTASQVIHRVGF-SSFGLLKL						-285
212-	IQRKKVHV-----FGDELSVTLFRCIQNMPETL-----P--NNSCYASAGIARLEEGDEIQLAIPRENAQISLDGDTVTFGALKLL						-309
236-	IQRKKVHV-----FGDELSVTLFRCIQNMPKTL-----P--NNSCYASAGIARLEEGDEIQLAIPRENAQISLDGDTVTFGALKLL						-316
234-	YLQLMVYVTKTSI--KIPSSHNLMKGGSTKNWSGN-----SE--FHFYSINVGFFFKLRAGEEISIQVSNPSLLDPDQDA-TYFGAFKVDID						-317
235-	YLQLMVYVTKTSI--KIPSSHNLMKGGSTKNWSGN-----SE--FHFYSINVGFFFKLRAGEEISIEVSNPSLLDPDQDA-TYFGAFKVRDID						-281
201-	K-NDKQMVQYIYKTSYDPDPIVLMKSARNSCWSKD-----AE--YGLYSIYQGQIFELKENDRIFVSVTNEHLIDMDHEA-SFFGAFLV						-291
210-	KVRTKQLVQYIYKTSYDPDPIVLMKSARNSCWSKD-----AE--YGLYSIYQGQIFELKENDRIFVSVTNEHLIDMDHEA-SFFGAFLIN						-234
159-	KLELLIN-----KHKKQALVTVCESGMQTK--HVYQNLSQLLDYLVQVNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD						-239
164-	TLQLLIN-----SKIKKQTLVTVCESGVQSK--NIYQNLSQLLDYLVQVNTTISVNVDTFQYIDTSTFPLENVLSVFLYSSSD						-244
158-	TLRSSLYRAGGA--YGPGTPELLEGAETVTPVLDPARRQGYGPIWYTSVGFGLVQLRRGERVYVNIISHPDMVDFAHGK-TFFGAVMVG						-306
223-	TLRSALYRAGGA--YGRGSPPELLLEGAETVTPVVDPI---GYGSLWYTSVGFGLAQLRSGERVYVNIISHPDMVDYRAGK-TFFGAVMVG						-205
132-	AHEVQLFSS-----QYPFHVPLLSQKMVP-----GLQEPWLHSMYHGAAFQLTQGDQLSTHTDGIPLHLVLSPT-VFFGAFAL						-202
129-	AHEVQLFSS-----QYPFHVPLLSQKSVYP-----GLQGPWVRSMYQGAFFLLSKGDQLSTHTDGIHLHFSFS-S-VFFGAFAL						-233
153-	THTISRIV-----SYQTKVNLLSAIKSPQRETPEG--AEAKPWYEPYIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIALL						-235
155-	THTVSRFAI-----SYQEKVNLLSAVKSPKDTPEG--AELKPWYEPYIYLGGVFQLEKGDQLSAEINLPKYLDFAESGQVYFGVIAL						
							Consensus
							Human FasL
							Mouse FasL
							Rat FasL
							Human CD40L
							Mouse CD40L
							Human AGP3
							Mouse AGP3
							Mouse OPGL
							Human OPGL
							Human TRAIL
							Mouse TRAIL
							Human CD30L
							Mouse CD30L
							Human LyTb
							Mouse LyTb
							Human TNFb
							Mouse TNFb
							Human TNFa
							Mouse TNFa

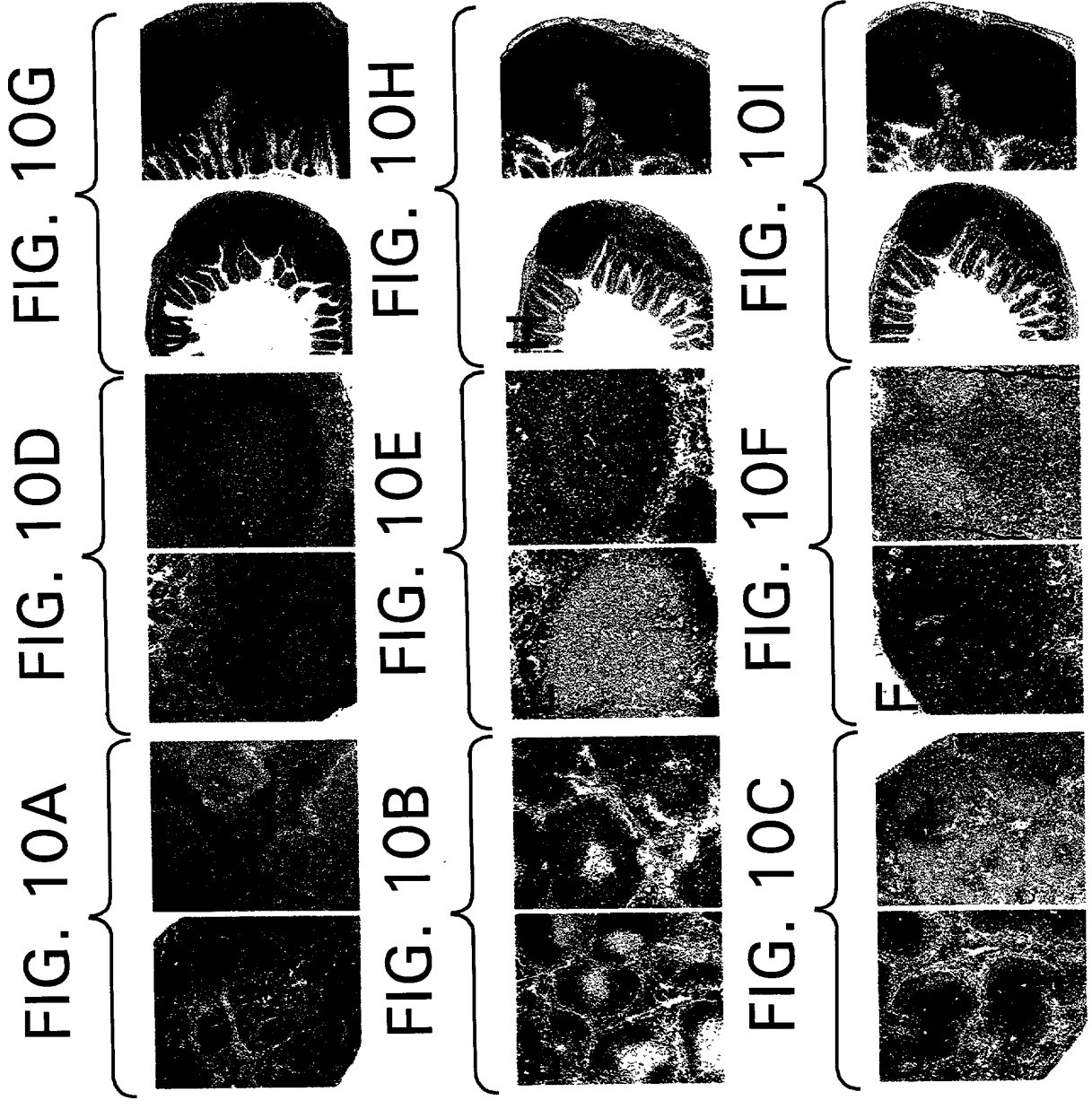


FIG. 11A

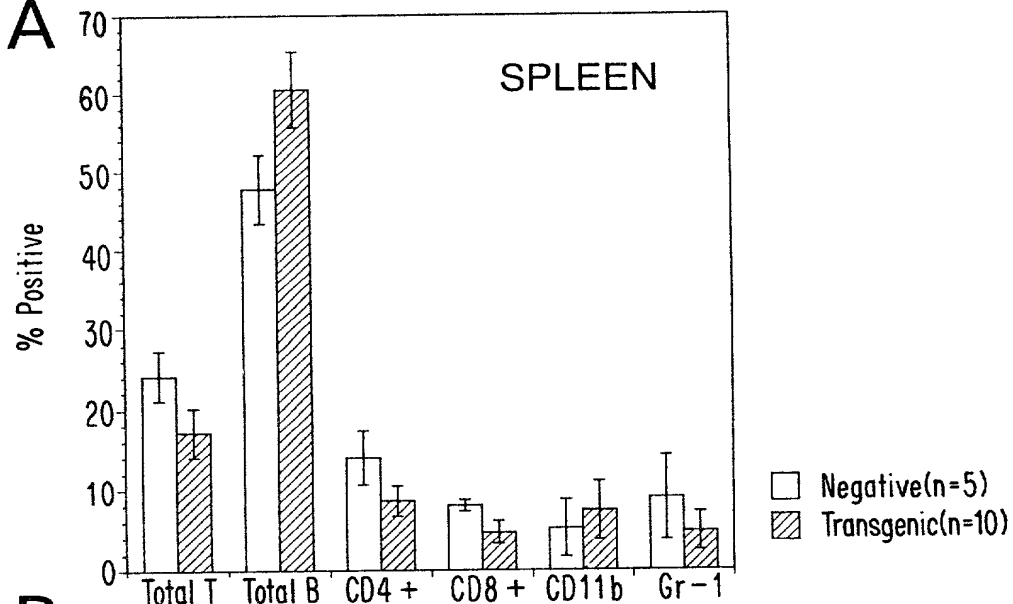


FIG. 11B

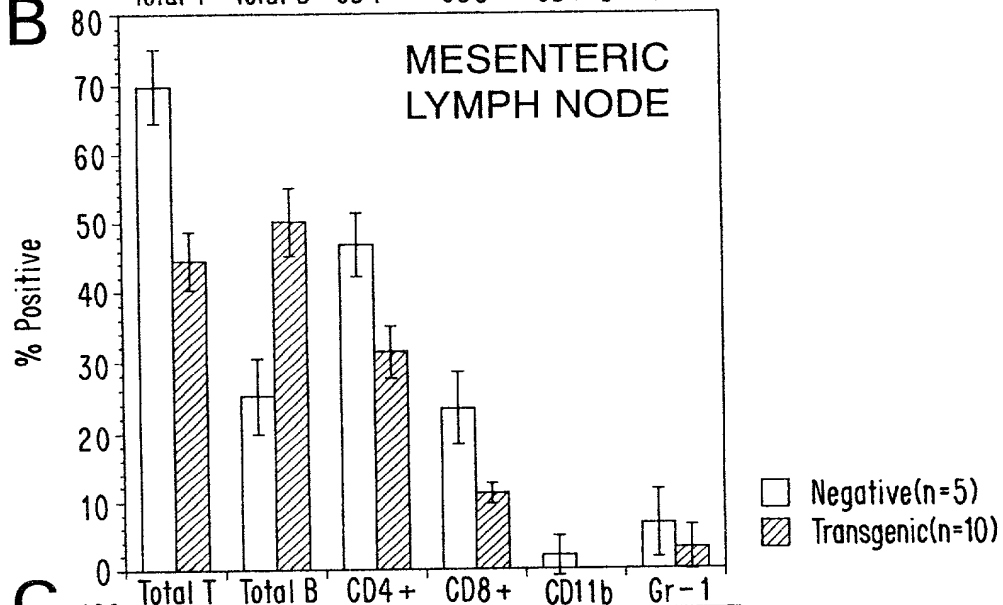


FIG. 11C

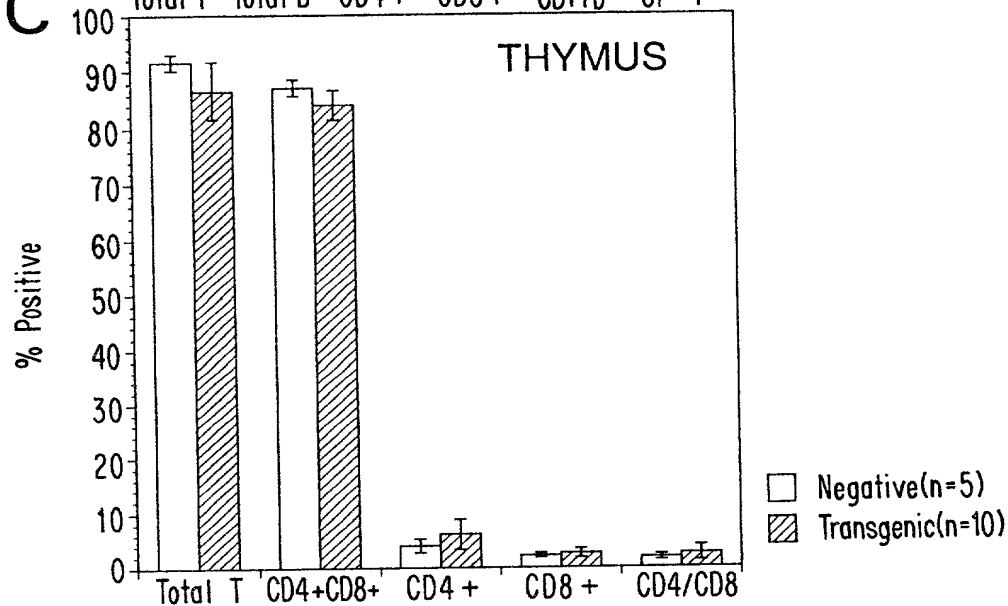


FIG. 12A

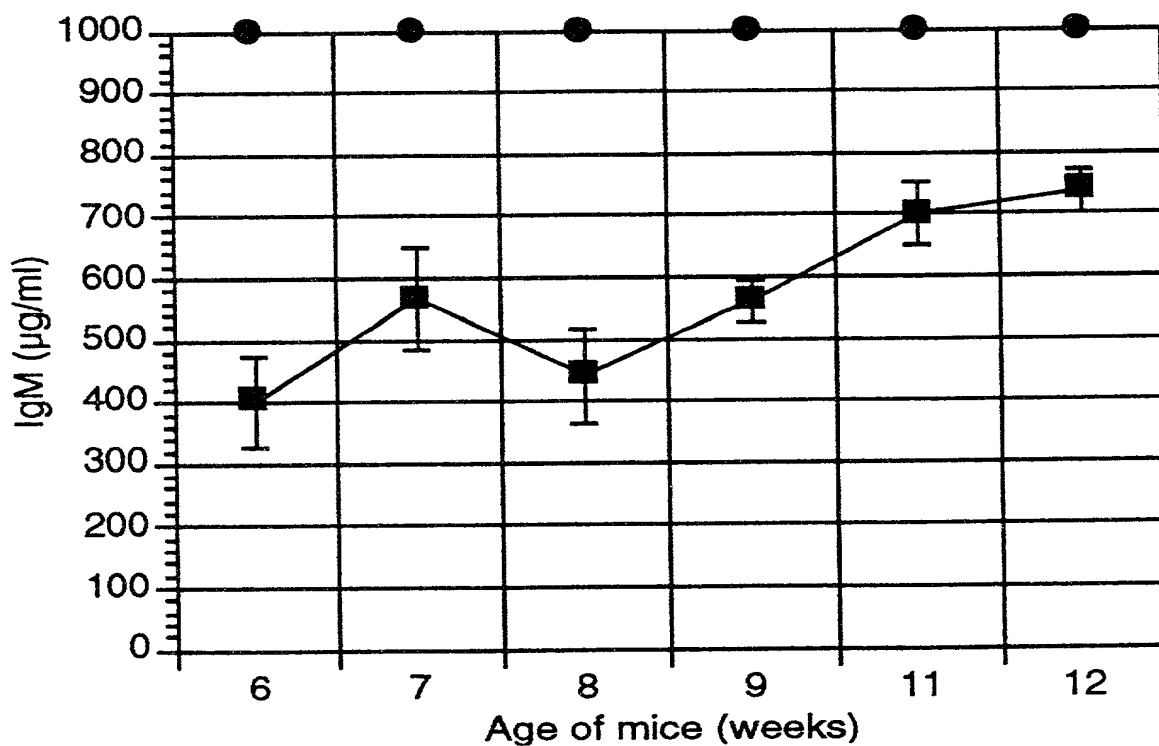


FIG. 12B

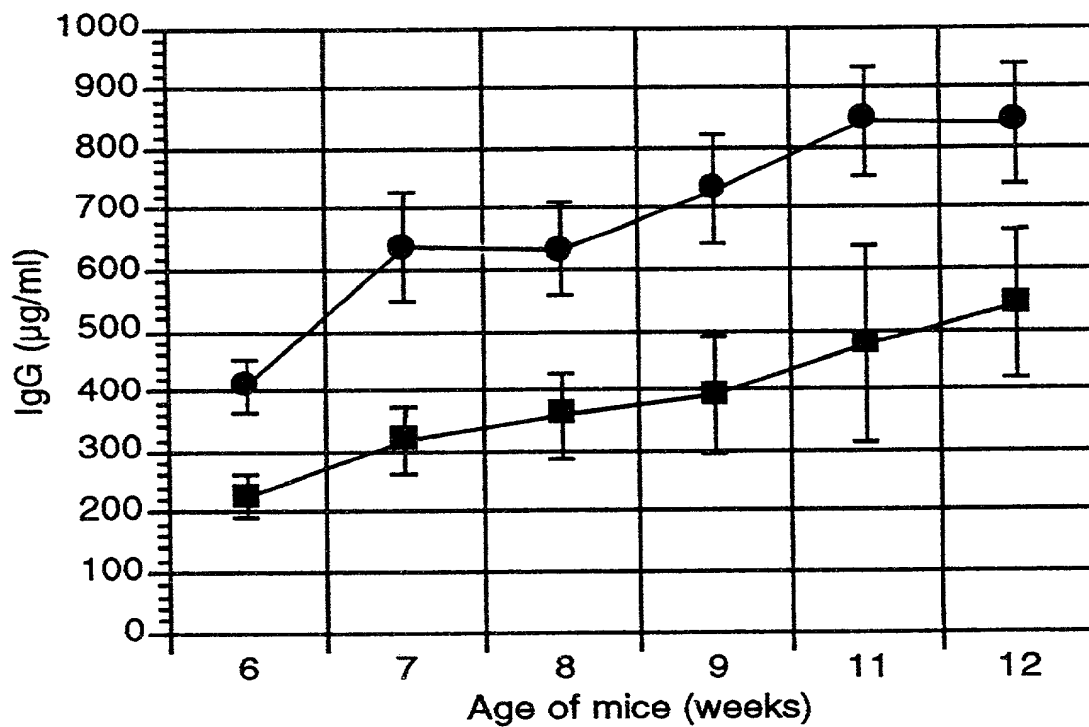


FIG. 12C

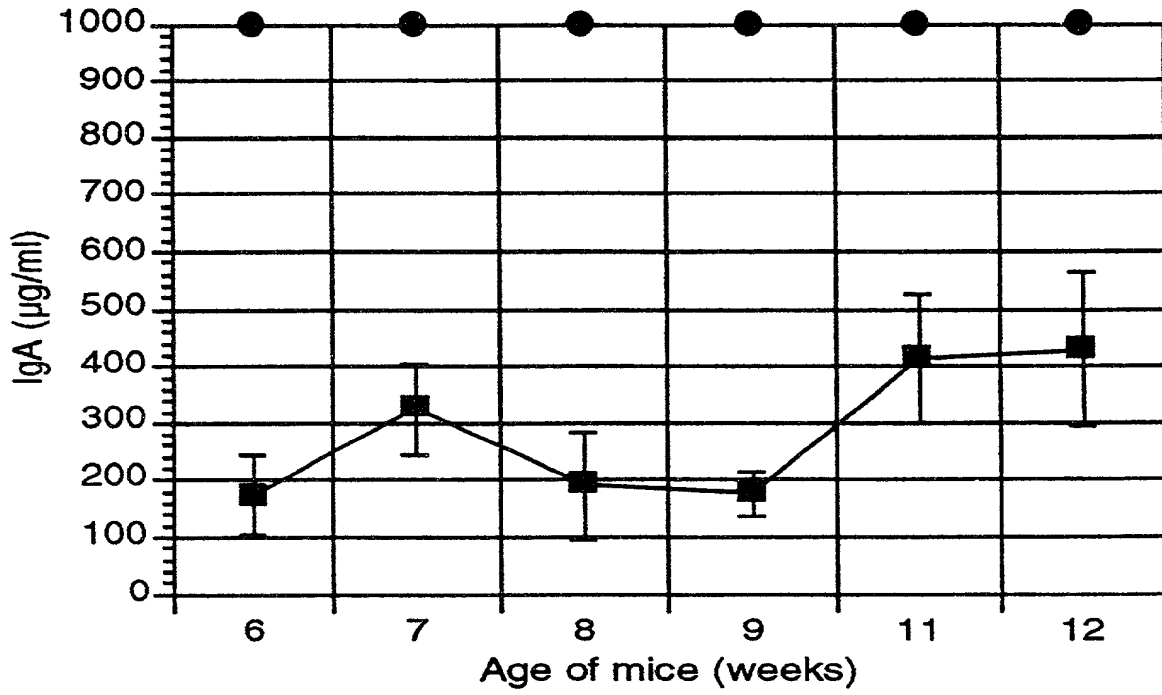


FIG. 12D

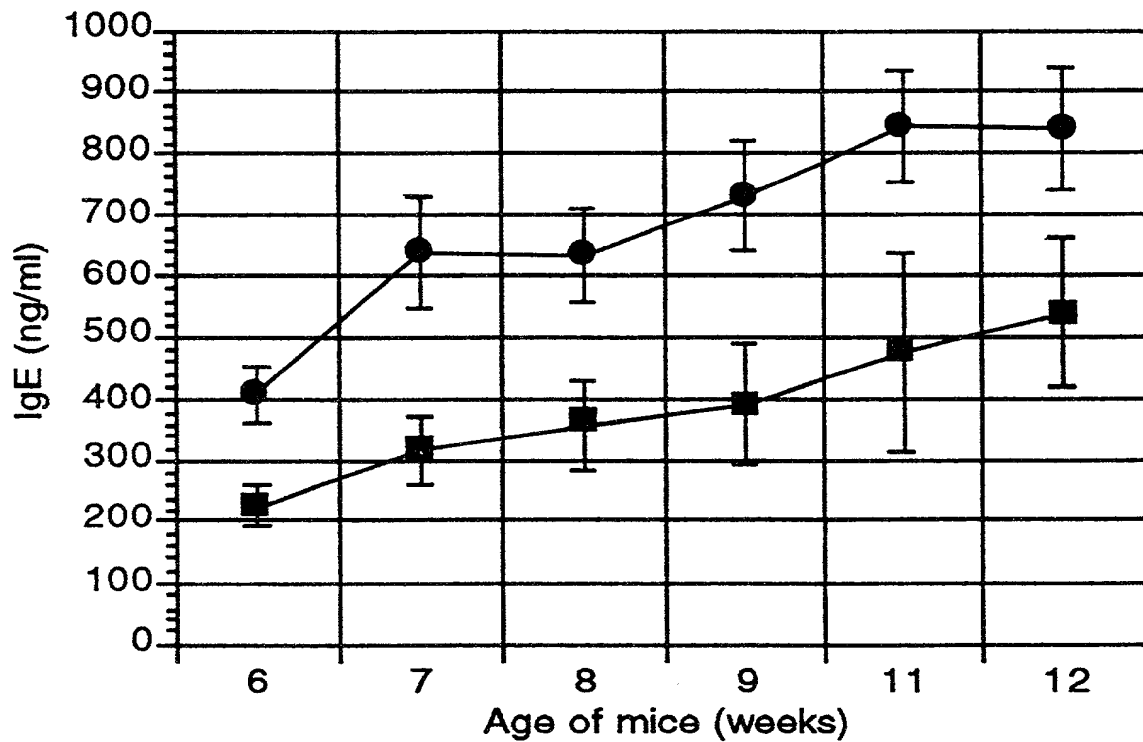


FIG. 13A

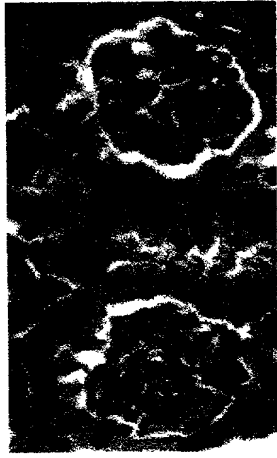


FIG. 13D



FIG. 13G

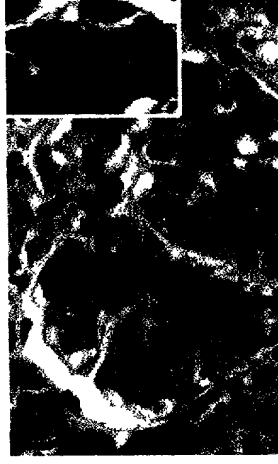


FIG. 13B



FIG. 13E

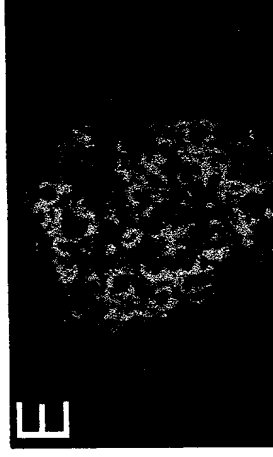


FIG. 13H

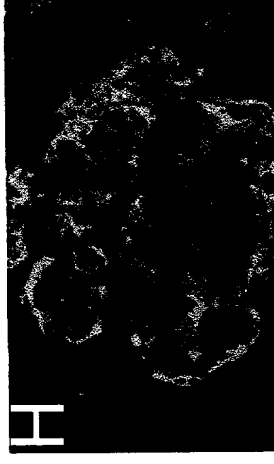


FIG. 13C

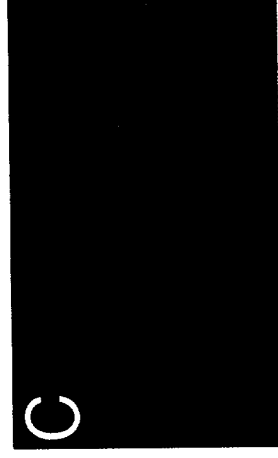


FIG. 13F

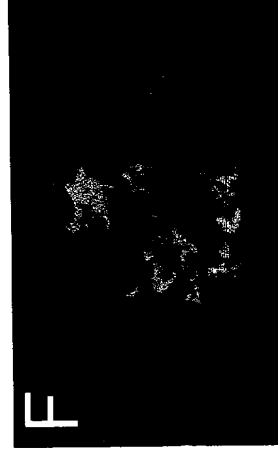


FIG. 13I

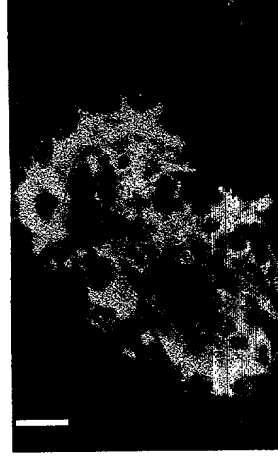


FIG. 14A

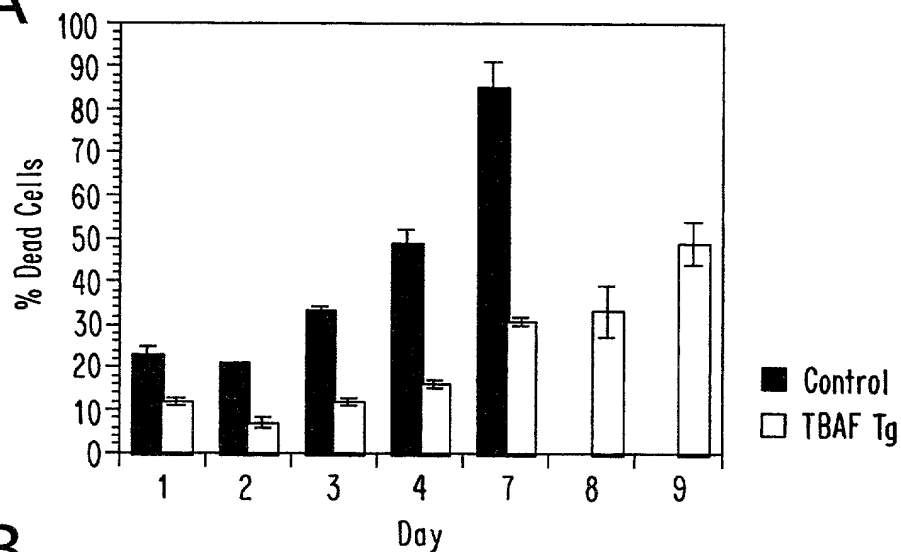


FIG. 14B

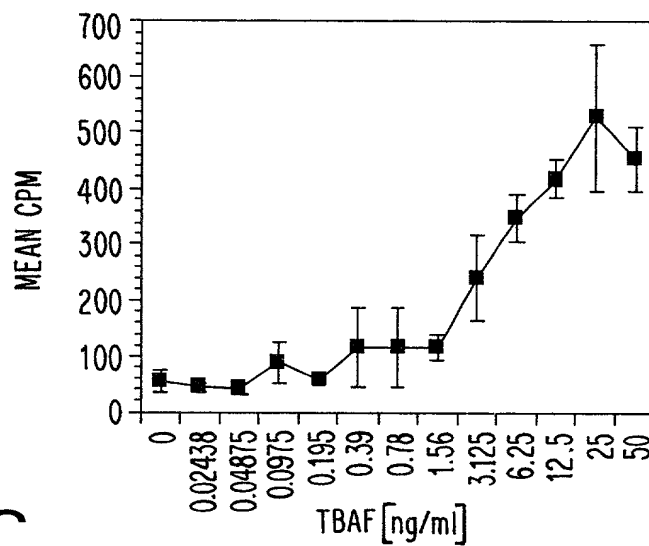


FIG. 14C

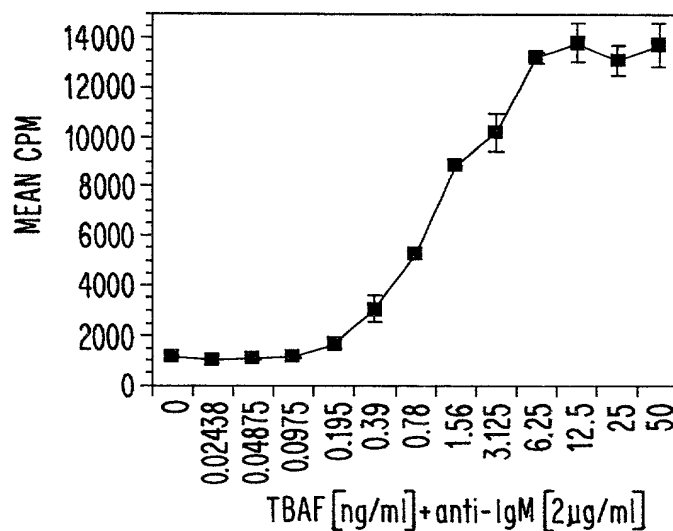


FIG. 15

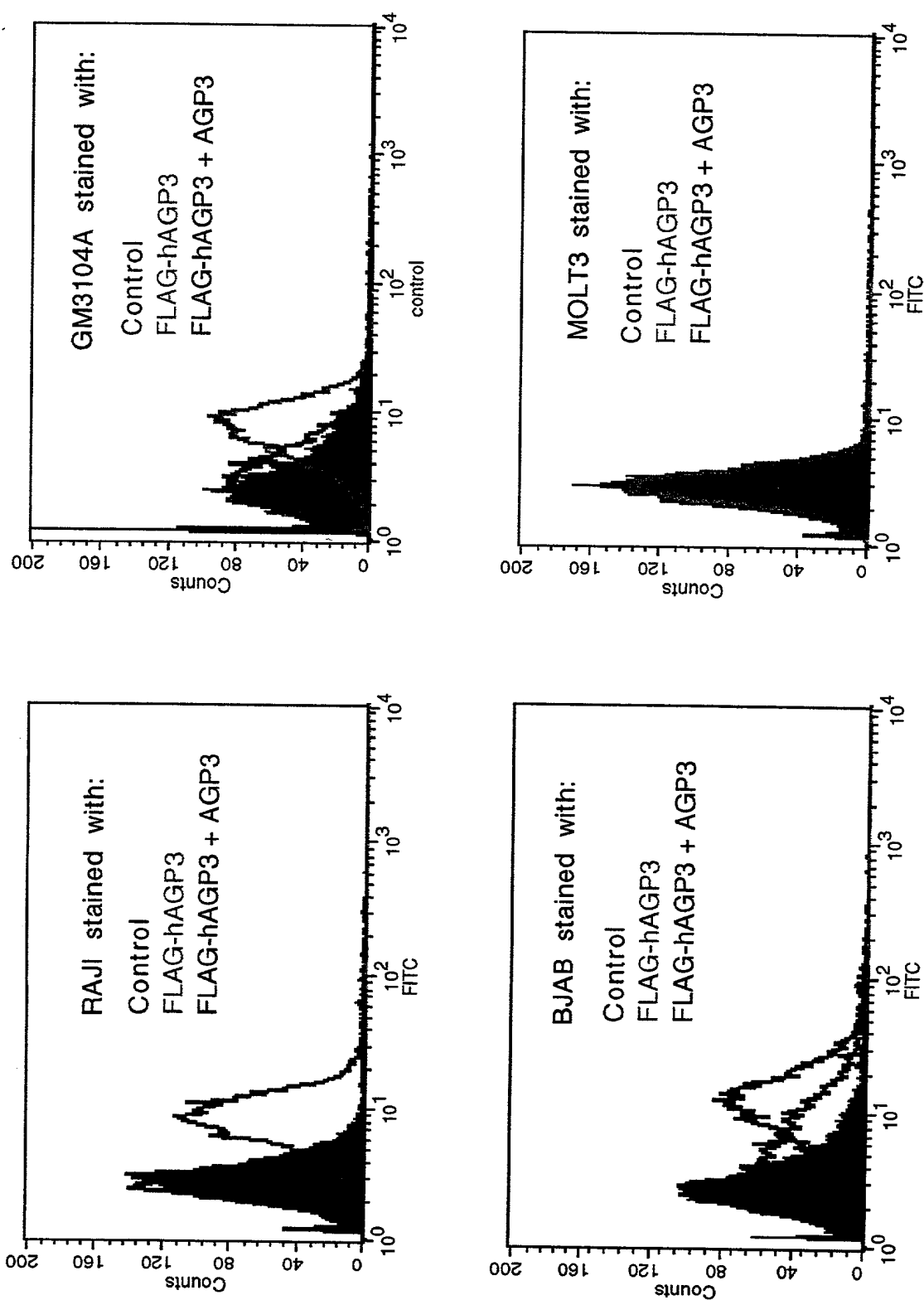


FIG. 16

Alignment of AGP3-binding pools 13B4 and 13H11
N-terminal sequence

1 GTCGACCCACGCGTCCG.....ATCCTGAGTAATGAGTGGCCTGGGCC 43
|||||
1 GTCGACCCACGCGTCCGAATAAGCATCCTGAGTAATGAGTGGCCTGGGCC 50
44 GGAGCAGGCGAGGTGGCCGGAGCCGTGTGGACCAGGAGGAGCGCTTTCCA 93
|||||
51 GGAGCAGGCGAGGTGGCCGGAGCCGTGTGGACCAGGAGGAGCGCTTTCCA 100
94 CAGGGCCTGTGGACAGGGGTGGCTATGAGATCCTGCCCCGAAGAGCAGTA 143
|||||
101 CAGGGCCTGTGGACAGGGGTGGCTATGAGATCCTGCCCCGAAGAGCAGTA 150
144 CTGGGATCCTCTGCTGGGTACCTGCATGTCCTGCAAAACCATTGTGCAACC 193
|||||
151 CTGGGATCCTCTGCTGGGTACCTGCATGTCCTGCAAAACCATTGTGCAACC 200
194 ATCAGAGCCAGCGCACCTGTGCAGCCTTCTGCAGGTCACTCAGCTGCCGC 243
|||||
201 ATCAGAGCCAGCGCACCTGTGCAGCCTTCTGCAGGTCACTCAGCTGCCGC 250
244 AAGGAGCAAGGCAAGTTCTATGACCATCTCCTGAGGGACTGCATCAGCTG 293
|||||
251 AAGGAGCAAGGCAAGTTCTATGACCATCTCCTGAGGGACTGCATCAGCTG 300
294 TGCCTCCATCTGTGGACAGCACCTAAGCAATGTGCATACTTCTGTGAGA 343
|||||
301 TGCCTCCATCTGTGGACAGCACCTAAGCAATGTGCATACTTCTGTGAGA 350
344 ACAAGCTCAGGAGCCCAGTGAACCTTCCACCAGAGCTCAGGAGACAGCGG 393
|||||
351 ACAAGCTCAGGAGCCCAGTGAACCTTCCACCAGAGCTCAGGAGACAGCGG 400

FIG. 17

Human AGP3 receptor sequence

GTCTGACCCACGCGTCCGATCCTGAGTAATGAGTGGCCTGGGCCGGAGCAGGCGAGGTGGC
M S G L G R S R R G G
CGGAGCCGTGTGGACCAGGAGGAGCGCTTCCACAGGGCCTGTGGACAGGGGTGGCTATG
R S R V D Q E E R F P Q G L W T G V A M
AGATCCTGCCCCGAAGAGCAGTACTGGGATCCTCTGCTGGGTACCTGCATGTCCTGCAAA
R S C P E E Q Y W D P L L G T C M S C K
ACCATTGCAACCATCAGAGCCAGCGCACCTGTGCAGCCTTCTGCAGGTCACTCAGCTGC
T I C N H Q S Q R T C A A F C R S L S C
CGCAAGGAGCAAGGCAAGTTCTATGACCATCTCCTGAGGGACTGCATCAGCTGTGCCTCC
R K E Q G K F Y D H L L R D C I S C A S
ATCTGTGGACAGCACCTAAGCAATGTGCATACTTCTGTGAGAACAGCTCAGGAGCCCA
I C G Q H P K Q C A Y F C E N K L R S P
GTGAACCTTCCACCAGAGCTCAGGAGACAGCGGAGTGGAGAAGTTGAAAACAATTGAGAC
V N L P P E L R R Q R S G E V E N N S D
AACTCGGGAAGGTACCAAGGACTGGAGCACAGAGGCTCAGAAGCAAGTCCAGCTCTCCCG
N S G R Y Q G L E H R G S E A S P A L P
GGGCTGAAGCTGAGTGCAGATCAGGTGGCCCTGGTCTACAGCACGCTGGGGCTCTGCCTG
G L K L S A D Q V A L V Y S T L G L C L
TGTGCCGTCCTCTGCTGCTTCTGGTGGCGGTGGCCTGCTTCTCAAGATGAGGGGGGAT
C A V L C C F L V A V A C F L K M R G D
CCCTGCTCCTGCCAGCCCCGCTCAAGGCCCGTCAAAGTCCGGCCAAGTCTTCCAGGAT
P C S C Q P R S R P R Q S P A K S S Q D
CACGCGATGGAAGCCGGCAGCCCTGTGAGCACATCCCCGAGCCAGTGGAGACCTGCAGC
H A M E A G S P V S T S P E P V E T C S
TTCTGCTTCCCTGAGTGCAGGGCGCCACGCAGGAGAGCGCAGTCACGCCTGGGACCCCC
F C F P E C R A P T Q E S A V T P G T P
GACCCCACTTGTGCTGGAAGGTGGGGGTGCCACACCAGGACCACAGTCCTGCAGCCTTGC
D P T C A G R W G C H T R T T V L Q P C
CCACACATCCCAGACAGCGGCCCTTGGCATTGTGTGTGTGCCTGCCAGGAGGGGGGCCCA
P H I P D S G L G I V C V P A Q E G G P
GGTGCATAAATGGGGGTCAGGGAGGGAAGGAGGAGGAGAGATGGAGAGGAGGGGAG
G A
AGAGAAAGAGAGGTGGGGAGAGGGGAGAGAGATATGAGGAGAGAGAGACAGAGGAGGCAG
AGAGGGAGAGAAACAGAGGAGACAGAGAGGGAGAGAGACAGAGGGAGAGAGAGACAGA
GAGGAAGAGAGGCAGAGAGGGAAAGAGGCAGAGAAGGAAAGAGACAGGCAGAGAAGGAGA
GAGGCAGAGAGGGAGAGAGGCAGAGAGGGAGAGAGGCAGAGAGACAGAGAGGGAGAGAGG
GACAGAGAGAGATAGAGCAGGAGGTGGGGCACTCTGAGTCCCAGTCCCAGTGCAGCTG
TAGGTCGTCATCACCTAACCAACAGTGCATAAAGTCCTCGTGCCTGCTGCTCACAGCCC
CCGAGAGCCCCCTCCTCCTGG

FIG. 18

AGP3 receptor protein structure

MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMR

SCPEEQYWDPLLGTCTMSCKTICNHQSQRRTCAAFCRSL I

SCRKEQGKFYDHLLRDCISCASICGQHPKQCAVFCENK II

LRSPVNLPPPELRRQRSGEVENNSDNGRYQGLEHRGSE stalk
ASPALPGLKLSADQVAVYS

TLGLCLCAVLCCFLVAVACFL TM

KMRGDPCSCQPRSRPRQSPAKSSQDHAMEAGSPVSTSP IC
EPVETCSFCFPECRAPTQESAVTPGTPDTCAGRWCHT
RTTVLQPCPHIPDSGLGIVCVPAQEGGPGA

FIG. 19

Alignment of AGP3 receptor and TNFR1 extracellular domain

10	20	30	40	50	60	
LGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTTCMSCKTICNHQS-QR						AGP3R
: : : : : : :						
20	30	40	50	60	70	
VLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNNSIC--C-TKCHKGTLYN						TNFR1
70	80	90	100	110		
TCAAFCRSLSCRK-EQGKF-YDHLLRDCISCASICGQHPKQCAYFCENKLRSVPVNLPPPE						AGP3R
: : : : : : : : : : : :						
80	90	100	110	120		
DCPGPGQDTCRECESGSFTASENHLRHCLSC-SKCRKEMGQVEISSCTVDRDRTVCGCRK						TNFR1

FIG. 20

Human AGP3 receptor mRNA tissue distribution

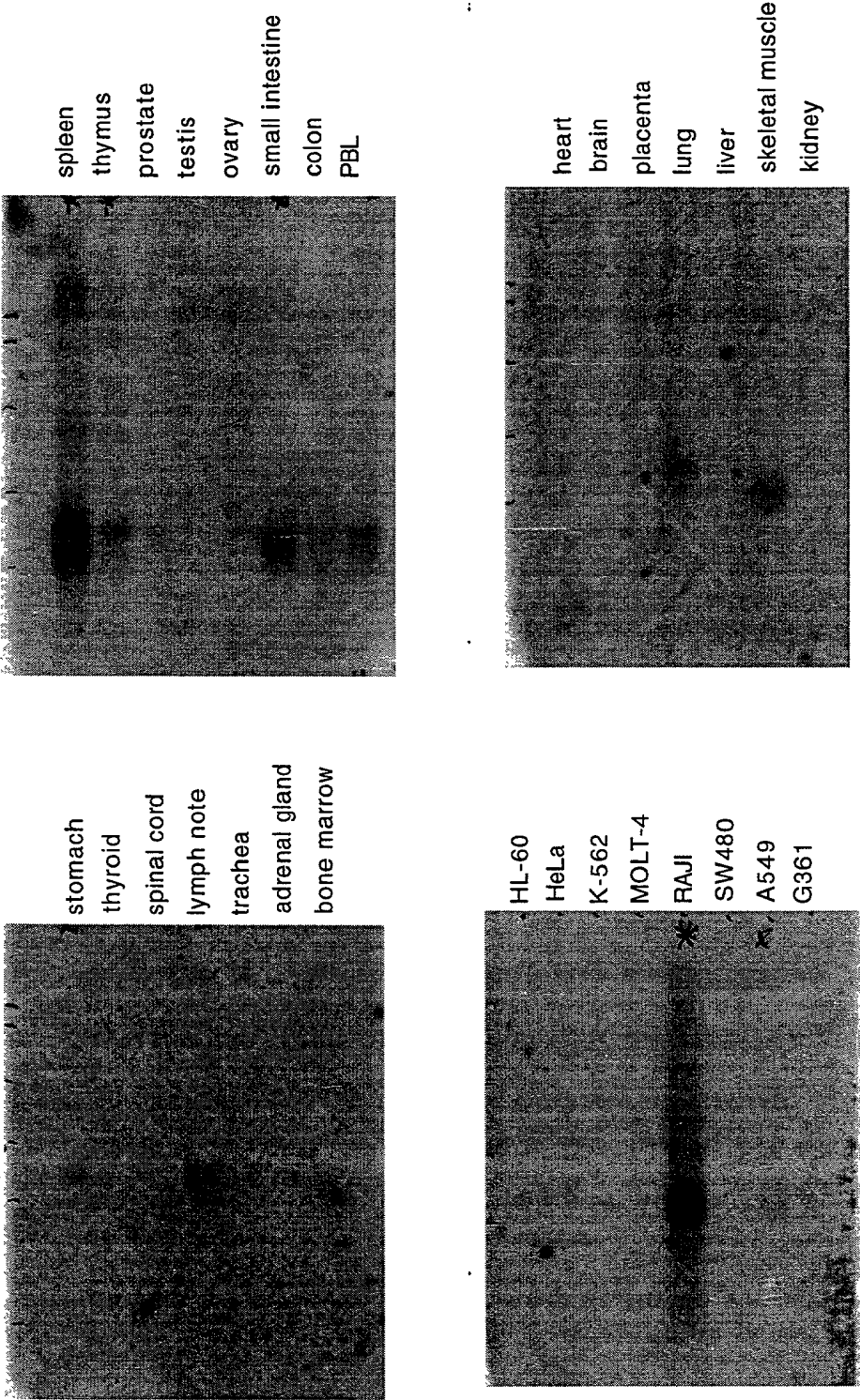


FIG 21

